

#8

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

Metz, James G.
Lardizabal, Kathryn D.
Lassner, Michael

(ii) TITLE OF INVENTION: Nucleic Acid Sequences Encoding in A
Cytoplasmic Protein Involved in Fatty Acyl-COA Metabolism

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Calgene, Inc.

(B) STREET: 1920 Fifth Street

(C) CITY: Davis

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 95616

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: Macintosh 7.0

(D) SOFTWARE: Microsoft Word 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/657,749

(B) FILING DATE: 30-MAY-96

(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/13686

(B) FILING DATE: 30-NOV-94

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/265,047

(B) FILING DATE: 23-JUN-94

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/160,602

(B) FILING DATE: 30-NOV-93

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/066,299

(B) FILING DATE: 20-MAY-93

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US92/09863

(B) FILING DATE: 13-NOV-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/933,411

(B) FILING DATE: 21-AUG-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/796,256

(B) FILING DATE: 20-NOV-91

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (916) 753-6313

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(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAATCCTCCA CTCATACACT CCACCTCTCT CTCTCTCTCT AACAAATTGA	60
GTAGCAAAC TAAAAGAAA ATG GAG GAA ATG GGA AGC ATT TTA GAG TTT CTT	112
Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu	
1 5 10	
GAT AAC AAA GCC ATT TTG GTC ACT GGT GCT ACT GGC TCC TTA GCA AAA	160
Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys	
15 20 25	
ATT TTT GTG GAG AAG GTA CTG AGG AGT CAA CCG AAT GTG AAG AAA CTC	208
Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu	
30 35 40	
TAT CTT CTT TTG AGA GCA ACC GAT GAC GAG ACA GCT GCT CTA CGC TTG	256
Tyr Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu	
45 50 55	
CAA AAT GAG GTT TTT GGA AAA GAG TTG TTC AAA GTT CTG AAA CAA AAT	304
Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn	
60 65 70 75	
TTA GGT GCA AAT TTC TAT TCC TTT GTA TCA GAA AAA GTG ACT GTA GTA	352
Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val	
80 85 90	

AGC ACT TTT AAA GAG CCC TTT CCT GGT TGG GTT GAA GGT GTC AGG ACC Ser Thr Phe Lys Glu Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr 270 275 280	928
ATC GAT AAT GTA CCT GTA TAT TAT GGT AAA GGG AGA TTG AGG TGT ATG Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met 285 290 295	976
CTT TGC GGA CCC AGC ACA ATA ATT GAC CTG ATA CCG GCA GAT ATG GTC Leu Cys Gly Pro Ser Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val 300 305 310 315	1024
GTG AAT GCA ACG ATA GTA GCC ATG GTG GCG CAC GCA AAC CAA AGA TAC Val Asn Ala Thr Ile Val Ala Met Val Ala His Ala Asn Gln Arg Tyr 320 325 330	1072
GTA GAG CCG GTG ACA TAC CAT GTG GGA TCT TCA GCG GCG AAT CCA ATG Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met 335 340 345	1120
AAA CTG AGT GCA TTA CCA GAG ATG GCA CAC CGT TAC TTC ACC AAG AAT Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn 350 355 360	1168
CCA TGG ATC AAC CCG GAT CGC AAC CCA GTA CAT GTG GGT CGG GCT ATG Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met 365 370 375	1216
GTC TTC TCC TCC TTC TCC ACC TTC CAC CTT TAT CTC ACC CTT AAT TTC Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe 380 385 390 395	1264
CTC CTT CCT TTG AAG GTA CTG GAG ATA GCA AAT ACA ATA TTC TGC CAA Leu Leu Pro Leu Lys Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln 400 405 410	1312
TGG TTC AAG GGT AAG TAC ATG GAT CTT AAA AGG AAG ACG AGG TTG TTG Trp Phe Lys Gly Lys Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu 415 420 425	1360
TTG CGT TTA GTA GAC ATT TAT AAA CCC TAC CTC TTC TTC CAA GGC ATC Leu Arg Leu Val Asp Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile 430 435 440	1408

TTT GAT GAC ATG AAC ACT GAG AAG TTG CGG ATT GCT GCA AAA GAA AGC 1456
Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser
445 450 455

ATA GTT GAA GCT GAT ATG TTT TAC TTT GAT CCC AGG GCA ATT AAC TGG 1504
Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp
460 465 470 475

GAA GAT TAC TTC TTG AAA ACT CAT TTC CCA GGN GTC GTA GAG CAC GTT 1552
Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
480 485 490

CTT AAC TAAAAGTTAC GGTACGAAAA TGAGAAGATT GGAATGCATG CACCGAAAGN 1608
Leu Asn

NCAACATAAA AGACGTGGTT AAAGTCATGG TCAAAAAAGA AATAAAATGC AGTTAGGTTT 1668

GTGTTGCAGT TTTGATTCCCT TGTATTGTTA CTTGTACTTT TGATCTTTTT CTTTTTTAAT 1728

GAAATTTCTC TCTTGTTTT GTGAAAAAAA AAAAAAAA GAGCTCCTGC AGAAGCTT 1786

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2 :

GGAACTCCAT CCCTTCCTCC CTCACTCCTC TCTCTACA ATG AAG GCC AAA ACA ATC 56
Met Lys Ala Lys Thr Ile
1 5

ACA AAC CCG GAG ATC CAA GTC TCC ACG ACC ATG ACC ACC ACG ACC ACG 104
Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr
10 15 20

ACT ATG ACC GCC ACT CTC CCC AAC TTC AAG TCC TCC ATC AAC TTA CAC		152
Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His		
25	30	35
CAC GTC AAG CTC GGC TAC CAC TAC TTA ATC TCC AAT GCC CTC TTC CTC		200
His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu		
40	45	50
GTA TTC ATC CCC CTT TTG GGC CTC GCT TCG GCC CAT CTC TCC TCC TTC		248
Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His Leu Ser Ser Phe		
55	60	65
70		
TCG GCC CAT GAC TTG TCC CTG CTC TTC GAC CTC CTT CGC CGC AAC CTC		296
Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu		
75	80	85
CTC CCT GTT GTC GTT TGT TCT TTC CTC TTC GTT TTA TTA GCA ACC CTA		344
Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu		
90	95	100
CAT TTC TTG ACC CGG CCC AGG AAT GTC TAC TTG GTG GAC TTT GGA TGC		392
His Phe Leu Thr Arg Pro Arg Asn Val Tyr Leu Val Asp Phe Gly Cys		
105	110	115
TAT AAG CCT CAA CCG AAC CTG ATG ACA TCC CAC GAG ATG TTC ATG GAC		440
Tyr Lys Pro Gln Pro Asn Leu Met Thr Ser His Glu Met Phe Met Asp		
120	125	130
CGG ACC TCC CGG GCC GGG TCG TTT TCT AAG GAG AAT ATT GAG TTT CAG		488
Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys Glu Asn Ile Glu Phe Gln		
135	140	145
150		
AGG AAG ATC TTG GAG AGG GCC GGT ATG GGT CGG GAA ACC TAT GTC CCC		536
Arg Lys Ile Leu Glu Arg Ala Gly Met Gly Arg Glu Thr Tyr Val Pro		
155	160	165
GAA TCC GTC ACT AAG GTG CCC GCC GAG CCG AGC ATA GCA GCA GCC AGG		584
Glu Ser Val Thr Lys Val Pro Ala Glu Pro Ser Ile Ala Ala Ala Arg		
170	175	180

GCC GAG GCG GAG GAG GTG ATG TAC GGG GCG ATC GAC GAG GTG TTG GAG Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu 185 190 195	632
AAG ACG GGG GTG AAG CCG AAG CAG ATA GGA ATA CTG GTG GTG ANC TGC Lys Thr Gly Val Lys Pro Lys Gln Ile Gly Ile Leu Val Val Xxx Cys 200 205 210	680
AGC TTG TTT AAC CCA ACG CCG TCG CTG TCA TCC ATG ATA GTT AAC CAT Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His 215 220 225 230	728
TAC AAG CTN AGG GGT AAT ATA CTT AGC TAT AAT CTT GGT GGC ATG GGT Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly 235 240 245	776
TGC AGT GCT GGG CTC ATT TCC ATT GAT CTT GCC AAG GAC CTC CTA CAG Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala Lys Asp Leu Leu Gln 250 255 260	824
GTT TAC CGT AAA AAC ACA TAT GTG TTA GTA GTG AGC ACG GAA AAC ATG Val Tyr Arg Lys Asn Thr Tyr Val Leu Val Val Ser Thr Glu Asn Met 265 270 275	872
ACC CTT AAT TGG TAC TGG GGC AAT GAC CGC TCC ATG CTT ATC ACC AAC Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser Met Leu Ile Thr Asn 280 285 290	920
TGC CTA TTT CGC ATG GGT GGC GCT GCC ATC ATC CTC TCA AAC CGC TGG Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile Leu Ser Asn Arg Trp 295 300 305 310	968
CGT GAT CGT CGC CGA TCC AAG TAC CAA CTC CTT CAT ACA GTA CGC ACC Arg Asp Arg Arg Arg Ser Lys Tyr Gln Leu Leu His Thr Val Arg Thr 315 320 325	1016
CAC AAG GGC GCT GAC GAC AAG TCC TAT AGA TGC GTC TTA CAA CAA GAA His Lys Gly Ala Asp Asp Lys Ser Tyr Arg Cys Val Leu Gln Gln Glu 330 335 340	1064
GAT GAA AAT AAC AAG GTA GGT GTT GCC TTA TCC AAG GAT CTG ATG GCA Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser Lys Asp Leu Met Ala 345 350 355	1112

GTT GCC GGT GAA GCC CTA AAG GCC AAC ATC ACG ACC CTT GGT CCC CTC Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Leu Gly Pro Leu 360 365 370	1160
GTG CTC CCC ATG TCA GAA CAA CTC CTC TTC TTT GCC ACC TTA GTG GCA Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe Ala Thr Leu Val Ala 375 380 385 390	1208
CGT AAG GTC TTC AAG ATG ACG AAC GTG AAG CCA TAC ATC CCA GAT TTC Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe 395 400 405	1256
AAG TTG GCA GCG AAC GAC TTC TGC ATC CAT GCA GGA GGC AAA GCA GTG Lys Leu Ala Ala Asn Asp Phe Cys Ile His Ala Gly Gly Lys Ala Val 410 415 420	1304
TTG GAT GAG CTC GAG AAG AAC TTG GAG TTG ACG CCA TGG CAC CTT GAA Leu Asp Glu Leu Glu Lys Asn Leu Glu Leu Thr Pro Trp His Leu Glu 425 430 435	1352
CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC ACA TCG AGT AGC TCA Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser Ser Ser Ser 440 445 450	1400
TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA GGG AGG ATC CGT AAG Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg Ile Arg Lys 455 460 465 470	1448
GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn 475 480 485	1496
AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys 490 495 500	1544
AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys 505 510 515	1592

ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA 1640
Ile Ala Pro Ile Ala Ser
520

AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTA GTTGATGGGT GAGAACATGT 1700
CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG 1733

(2) INFORMATION FOR SEQ ID NO:3 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1783 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 :

GTCGACACA ATG AAG GCC AAA ACA ATC ACA AAC CCG GAG ATC CAA GTC TCC 51
Met Lys Ala Lys Thr Ile Thr Asn Pro Glu Ile Gln Val Ser
1 5 10

ACG ACC ATG ACC ACC ACG ACC GCC ACT CTC CCC AAC TTC AAG 99
Thr Thr Met Thr Thr Thr Ala Thr Leu Pro Asn Phe Lys
15 20 25 30

TCC TCC ATC AAC TTA CAC CAC GTC AAG CTC GGC TAC CAC TAC TTA ATC 147
Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile
35 40 45

TCC AAT GCC CTC TTC CTC GTA TTC ATC CCC CTT TTG GGC CTC GCT TCG 195
Ser Asn Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser
50 55 60

GCC CAC CTC TCC TCC TTC TCG GCC CAT GAC TTG TCC CTG CTC TTC GAC 243
Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
65 70 75

CTC CTT CGC CGC AAC CTC CTC CCC GTT GTC GTT TGT TCT TTC CTC TTC	291
Leu Leu Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe	
80 85 90	
GTT TTA TTA GCA ACC CTA CAT TTC TTG ACC CGG CCT AGG AAT GTC TAC	339
Val Leu Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr	
95 100 105 110	
TTG GTG GAC TTT GCC TGC TAT AAG CCT CAC CCG AAC CTG ATA ACA TCC	387
Leu Val Asp Phe Ala Cys Tyr Lys Pro His Pro Asn Leu Ile Thr Ser	
115 120 125	
CAC GAG ATG TTC ATG GAC CGG ACC TCC CGG GCC GGG TCG TTT TCT AAG	435
His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys	
130 135 140	
GAG AAT ATT GAG TTT CAG AGG AAG ATC TTG GAG AGG GCC GGT ATG GGC	483
Glu Asn Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly	
145 150 155	
CGG GAA ACC TAC GTC CCC GAA TCC GTC ACT AAG GTG CCG CCC GAG CCG	531
Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Pro Glu Pro	
160 165 170	
AGC ATA GCA GCA GCC AGG GCC GAG GCG GAG GAG GTG ATG TAC GGG GCG	579
Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala	
175 180 185 190	
ATC GAC GAG GTG TTG GAG AAG ACG GGG GTG AAG CCG AAG CAG ATA GGA	627
Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly	
195 200 205	
ATA CTG GTG GTG AAC TGC AGC TTG TTT AAC CCA ACG CCG TCG CTG TCA	675
Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser	
210 215 220	
TCC ATG ATA GTT AAC CAT TAC AAG CTT AGG GGT AAT ATA CTT AGC TAT	723
Ser Met Ile Val Asn His Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr	
225 230 235	
AAT CTT GGT GGC ATG GGT TGC AGT GCT GGG CTC ATT TCC ATT GAT CTT	771
Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu	
240 245 250	

GCC AAG GAC CTC CTA CAG GTT TAC CGT AAC ACA TAT GTG TTA GTA GTG Ala Lys Asp Leu Leu Gln Val Tyr Arg Asn Thr Tyr Val Leu Val Val	255 260 265 270	819
AGC ACA GAA AAC ATG ACC CTT AAT TGG TAC TGG GGC AAT GAC CGC TCC Ser Thr Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser	275 280 285	867
ATG CTT ATC ACC AAC TGC CTA TTT CGC ATG GGT GGC GCT GCC ATC ATC Met Leu Ile Thr Asn Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile	290 295 300	915
CTC TCA AAC CGC TGG CGT GAT CGT CGC CGA TCC AAG TAC CAA CTC CTT Leu Ser Asn Arg Trp Arg Asp Arg Arg Ser Lys Tyr Gln Leu Leu	305 310 315	963
CAC ACA GTA CGC ACC CAC AAG GGC GCT GAC GAC AAG TCC TAT AGA TGC His Thr Val Arg Thr His Lys Gly Ala Asp Asp Lys Ser Tyr Arg Cys	320 325 330	1011
GTC TTA CAA CAA GAA GAT GAA AAT AAC AAG GTA GGT GTT GCC TTA TCC Val Leu Gln Gln Glu Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser	335 340 345 350	1059
AAG GAT CTG ATG GCA GTT GCC GGT GAA GCC CTA AAG GCC AAC ATC ACG Lys Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr	355 360 365	1107
ACC CTT GGT CCC CTC GTG CTC CCC ATG TCA GAA CAA CTC CTC TTC TTT Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe	370 375 380	1155
GCC ACC TTA GTG GCA CGT AAG GTC TTC AAG ATG ACG AAC GTG AAG CCA Ala Thr Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro	385 390 395	1203
TAC ATC CCA GAT TTC AAG TTG GCA GCG AAG CAC TTC TGC ATC CAT GCA Tyr Ile Pro Asp Phe Lys Leu Ala Ala Lys His Phe Cys Ile His Ala	400 405 410	1251
GGA GGC AAA GCA GTG TTG GAT GAG CTC GAG ACG AAC TTG GAG TTG ACG Gly Gly Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr		1299

415

420

425

430

CCA TGG CAC CTT GAA CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC 1347
 Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn
 435 440 445

ACA TCG AGT AGC TCA TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA 1395
 Thr Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys
 450 455 460

GGG AGG ATC CGT AAG GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA 1443
 Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser
 465 470 475

GGT TTC AAG TGT AAC AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT 1491
 Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn
 480 485 490

CCG GCT AGA GAG AAG AAT CCT TGG ATG GAT GAA ATT GAG AAT TTC CCT 1539
 Pro Ala Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro
 495 500 505 510

GTC CAT GTG CCT AAA ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT 1592
 Val His Val Pro Lys Ile Ala Pro Ile Ala Ser
 515 520

TAGTAATGAA AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT 1652
 GAGAACATGT CTCATTGAGA ATAACGTGTG CATCGTTGTG TTGAATTGAT 1712
 TGGTGAAATT CTGTTAGAAT TGACGCATGA GTCATATATA TACAAATTAA AGTAAGATTT 1772
 TACGCTTCT T 1783

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1647 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: PCR to genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4 :

GGCGCGCCGG TACCTCTAGA CCTGGCGATT CAACGTGGTC GGATCATGAC GCTTCCAGAA	60
AACATCGAGC AAGCTCTCAA AGCTGACCTC TTTCGGATCG TACTGAACCC GAACAATCTC	120
GTTATGTCCC GTCGTCTCCG AACAGACATC CTCGTAGCTC GGATTATCGA CGAATCCATG	180
GCTATACCCA ACCTCCGTCT TCGTCACGCC TGGAACCCCTC TGGTACGCCA ATTCCGCTCC	240
CCAGAACGAA CCGGCGCCGA ATTGCGCGAA TTGCTGACCT GGAGACGGAA CATCGTCGTC	300
GGGTCCCTTGC GCGATTGCGG CGGAAGCCGG GTCGGGTTGG GGACGAGACC CGAATCCGAG	360
CCTGGTGAAG AGGTTGTTCA TCGGAGATT TAGACGGAG ATGGATCGAG CGGTTTGAG	420
GAAAGGGGAA GTGGGTTTGG CTCTTTGGA TAGAGAGAGT GCAGCTTGG AGAGAGACTG	480
GAGAGGTTA GAGAGAGACG CGGCGGATAT TACCGGAGGA GAGGCGACGA GAGATAGCAT	540
TATCGAAGGG GAGGGAGAAA GAGTGACGTG GAGAAATAAG AAACCGTTAA GAGTCGGATA	600
TTTATCATAT TAAAAGCCCCA ATGGGCCTGA ACCCATTAA ACAAGACAGA TAAATGGCC	660
GTGTGTTAAG TTAACAGAGT GTTAACGTTG GGTTCAAAT GCCAACGCCA TAGGAACAAA	720
ACAAACGTGT CCTCAAGTAA ACCCCTGCCG TTTACACCTC AATGGCTGCA TGGTGAAGCC	780
ATTAACACGT GGCGTAGGAT GCATGACGAC GCCATTGACA CCTGACTCTC TTCCCTCTC	840
TTCATATATC TCTAATCAAT TCAACTACTC ATTGTCATAG CTATTCGGAA AATACATACA	900
CATCCTTTTC TCTTCGATCT CTCTCAATTG ACAAGAAGCA AAGTCGACGG ATCCCTGCAG	960

TAAATTACGC CATGACTATT TTCATAGTCC AATAAGGCTG ATGTCGGGAG TCCAGTTAT 1020
GAGCAATAAG GTGTTTAGAA TTTGATCAAT GTTTATAATA AAAGGGGGAA GATGATATCA 1080
CAGTCTTTG TTCTTTTG CTTTGTTAA ATTTGTGTGT TTCTATTGT AACACCTCCTG 1140
TATATGTTGT ACTTCTTTCC CTTTTAAGT GGTATCGTCT ATATGGTAAA ACGTTATGTT 1200
TGGTCTTC CTTTCTCTGT TTAGGATAAA AAGACTGCAT GTTTATCTT TAGTTATATT 1260
ATGTTGAGTA AATGAACCTT CATAGATCTG GTTCCGTAGA GTAGACTAGC AGCCGAGCTG 1320
AGCTGAAC TG AACAGCTGGC AATGTGAACA CTGGATGCAA GATCAGATGT GAAGATCTCT 1380
AATATGGTGG TGGGATTGAA CATATCGTGT CTATATTTT GTTGGCATT AAGCTTTAAC 1440
ATAGATATAA CTGATGCAGT CATTGGTTCA TACACATATA TAGTAAGGAA TTACAATGGC 1500
AACCCAAACT TCAAAAACAG TAGGCCACCT GAATTGCCTT ATCGAATAAG AGTTGTTTC 1560
CCCCCACTTC ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG 1620
GCAGAACCTC TAGAGGTACC GGCGCGC 1647

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5 :

Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6 :

Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa
5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :

Glu Thr Tyr Val Pro Glu Glu Val Thr Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8 :

Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9 :

Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe
5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10 :

Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu
5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala
5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12 :

Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu
5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13 :

Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala
5 10 15

Xaa Ile Leu Lys Asp Ala Gly
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14 :

Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser
5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 :

17

AAYATHACNA CNYTNGG

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 :

17

SWRTTRCAYT TRAANCC

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17 :

GAA ATG AGT AGG TCT AGC GAA CAA GAT CTA CTC TCT ACC GAG ATT GTT Met Ser Arg Ser Ser Glu Gln Asp Leu Leu Ser Thr Glu Ile Val 1 5 10 15	48
AAC CGT GGG ATC GAA CCT TCC GGT CCA AAC GCC GGT TCA CCA ACG TTC Asn Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe 20 25 30	96
TCG GTC AGA GTC CGG AGA CGT TTA CCG GAT TTT CTT CAA TCC GTA AAC Ser Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn 35 40 45	144
TTG AAG TAC GTG AAA CTT GGT TAT CAC TAC CTC ATA AAC CAT GCG GTT Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val 50 55 60	192
TAC TTG GCG ACG ATA CCG GTT CTT GTG CTT GTG TTT AGT GCC GAA GTT Tyr Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val 65 70 75	240
GGG AGT TTA AGC GGA GAA GAG ATT TGG AAG AAG CTT TGG GAC TAT GAT Gly Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp 80 85 90 95	288
ATC GCA ACC GTC ATC GGA TTC TTC GGT GTC TTT GTC TTG ACC GTT TGC Ile Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys 100 105 110	336

GTC TAC TTC ATG TCT CGT CCA CGA TCT GTT TAT CTC ATT GAC TTC GCT Val Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala 115 120 125	384
TGT TTC AAG CCT TCC GAT GAA CTT AAG GTG ACA AGA GAA GAG TTC ATA Cys Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile 130 135 140	432
GAT CTA GCT AGA AAA TCA GGC AAG TTC GAC GAA GAG ATC CTC GGA TTC Asp Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe 145 150 155	480
AAG AAG AGG ATC CTT CAA GCC TCA GGA ATA GGC GAT GAA ACG TAC GTC Lys Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val 160 165 170 175	528
CCA AGA TCA ATC TCT TCG TCG GAA AAC ACA ACA ACG ATG AAA GAA GGT Pro Arg Ser Ile Ser Ser Glu Asn Thr Thr Thr Met Lys Glu Gly 180 185 190	576
CGT GAA GAA GCC TCG ATG ATG ATA TTC GGC GCA CTC GAC GAA CTC TTC Arg Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe 195 200 205	624
GAG AAG ACA CGT GTC AAA CCG AAA GAC GTA GGT GTC CTC GTG GTT AAC Glu Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn 210 215 220	672
TGC AGT ATC TTT AAC CCG ACT CCG TCA CTC TCC GCG ATG GTG ATT AAC Cys Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn 225 230 235	720
CAC TAC AAG ATG AGA GGG AAC ATA CTT AGC TAC AAC CTA GGA GGG ATG His Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met 240 245 250 255	768
GGT TGC TCA GCA GGA ATC ATA GCC GTT GAT CTT GCT CGT GAC ATG CTT Gly Cys Ser Ala Gly Ile Ile Ala Val Asp Leu Ala Arg Asp Met Leu 260 265 270	816
CAG TCT AAC CCG AAT AGT TAC GCG GTG GTT GTG AGT ACC GAG ATG GTT Gln Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val 275 280 285	864

GGG TAT AAT TGG TAC GTG GGA CGT GAC AAG TCA ATG GTT ATA CCT AAC Gly Tyr Asn Trp Tyr Val Gly Arg Asp Lys Ser Met Val Ile Pro Asn 290	295	300	912	
TGC TTC TTT AGG ATG GGT TGC TCC GCC GTT ATG CTG TCT AAC CGC CGC Cys Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg 305	310	315	960	
CGT GAC TTC CGC CAT GCT AAG TAC CGC CTT GAG CAC ATT GTC CGG ACT Arg Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr 320	325	330	335	1008
CAC AAG GCT GCC GAC GAC CGT AGC TTC AGG AGT GTG TAC CAG GAA GAA His Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu 340	345	350	1056	
GAT GAA CAA GGA TTC AAG GGA TTA AAA ATA AGC AGA GAC CTA ATG GAA Asp Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu 355	360	365	1104	
GTT GGA GGT GAA GCT CTC AAG ACC AAC ATC ACC ACC TTA GGC CCT CTC Val Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu 370	375	380	1152	
GTC CTT CCT TTC TCC GAG CAG CTT CTC TTC TTT GCC GCT TTG ATC CGT Val Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Ile Arg 385	390	395	1200	
AGA ACT TTC TCA CCC GCC GCC AAA ACT ACC ACC ACC TCC TCC TCA GCC Arg Thr Phe Ser Pro Ala Ala Lys Thr Thr Thr Ser Ser Ser Ala 400	405	410	415	1248
ACT GCG AAA ATC AAC GGA GCC AAG TCG TCA TCC TCC TCT GAT CTA TCC Thr Ala Lys Ile Asn Gly Ala Lys Ser Ser Ser Ser Ser Asp Leu Ser 420	425	430	1296	
AAG CCG TAC ATC CCG GAC TAC AAG CTT GCC TTC GAG CAT TTC TGC TTC Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys Phe 435	440	445	1344	
CAC GCG GCA AGC AAA GCG GTG CTT GAG GAG CTT CAG AAG AAT CTA GGC His Ala Ala Ser Lys Ala Val Leu Glu Glu Leu Gln Lys Asn Leu Gly 450	455	460	1392	

TTG AGT GAT GAG AAC ATG GAG GCT TCT AAG ATG ACT TTA CAC AGG TTT Leu Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe 465	470	475	1440
GGA AAC ACT TCC AGC AGT GGA ATC TGG TAC GAG CTT GCT TAC ATG GAG Gly Asn Thr Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met Glu 480	485	490	1488
GCC AAG GAG AGT GTT CGT AGA GGC GAT AGG GTT TGG CAG ATT GCT TTT Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala Phe 500	505	510	1536
GGG TCA GGT TTT AAG TGT AAC AGT GTG GTT TGG AAG GCA ATG AGG AAG Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg Lys 515	520	525	1584
GTG AAG AAG CCG GCA AGG AAC AAT CCT TGG GAT TGC ATT AAC CGT Val Lys Lys Pro Ala Arg Asn Asn Pro Trp Val Asp Cys Ile Asn Arg 530	535	540	1632
TAC CCT GTC GCT CTC TGATCATTAA TTTTTAAAAT TATTATTCT TCTTAATTAA Tyr Pro Val Ala Leu 545			1687

ATCATCTATG ATCTCTCTTC CTTGTTGTTG GATGATAGAC GTTGTGTTGC TGGTCATTG 1747
TATCTTAAGA CTTCTATAAG AATGGATGGT TCAAGTCCAA AAAAAAAAAA AAAAAAAAAA 1807
AAA 1810
(S) INFORMATION FOR SEQ ID NO: 18

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18 :

GTCGACAAA ATG ACG TCC ATT AAC G	T	A	A	G	C	T	T	T	A	C	T	T	A	C	T	G	T	A	T	A	51
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile																					
1																				10	
ACC AAC CTT TTC AAC CTT TGT TTC TTT CCA TTA ACG GCG ATC GTC GCC																				99	
Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala																					
15																				30	
GGA AAA GCC TAT CGG CTT ACC ATA GAC GAT CTT CAC CAC TTA TAC TAT																				147	
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr																					
35																				45	
TCC TAT CTC CAA CAC AAC CTC ATA ACC ATT GCT CCA CTC TTT GCC TTC																				195	
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe																					
50																				60	
ACC GTT TTC GGT TCG GTT CTC TAC ATC GCA ACC CGG CCC AAA CCG GTT																				243	
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val																					
65																				75	
TAC CTC GTT GAG TAC TCA TGC TAC CTT CCA CCA ACG CAT TGT AGA TCA																				291	
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser																					
80																				90	
AGT ATC TCC AAG GTC ATG GAT ATC TTT TAC CAA GTA AGA AAA GCT GAT																				339	
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp																					
95																				110	
CCT TCT CGG AAC GGC ACG TGC GAT GAC TCG TCC TGG CTT GAC TTC TTG																				387	
Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu																					
115																				125	
AGG AAG ATT CAA GAA CGT TCA GGT CTA GGC GAT GAA ACC CAC GGG CCC																				435	
Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro																					
130																				140	
GAG GGG CTG CTT CAG GTC CCT CCC CGG AAG ACT TTT GCG GCG GCG CGT																				483	
Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg																					
145																				155	

GAA GAG ACG GAG CAA GTT ATC ATT GGT GCG CTA GAA AAT CTA TTC AAG Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys 160 165 170	531
AAC ACC AAT GTT AAC CCT AAA GAT ATA GGT ATA CTT GTG GTG AAC TCA Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser 175 180 185 190	579
AGC ATG TTT AAT CCA ACT CCT TCG CTC TCC GCG ATG GTC GTT AAC ACT Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr 195 200 205	627
TTC AAG CTC CGA AGC AAC GTA AGA AGC TTT AAC CTT GGT GGC ATG GGT Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly 210 215 220	675
TGT AGT GCC GGC GTT ATA GCC ATT GAT CTA GCA AAG GAC TTG TTG CAT Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His 225 230 235	723
GTC CAT AAA AAT ACG TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr 240 245 250	771
TAT AAC ATT TAC GCT GGT GAT AAT AGG TCC ATG ATG GTT TCA AAT TGC Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys 255 260 265 270	819
TTG TTC CGT GTT GGT GGG GCC GCT ATT TTG CTC TCC AAC AAG CCT AGA Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg 275 280 285	867
GAT CGT AGA CGG TCC AAG TAC GAG CTA GTT CAC ACG GTT CGA ACG CAT Asp Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His 290 295 300	915
ACC GGA GCT GAC GAC AAG TCT TTT CGT TGC GTG CAA CAA GGA GAC GTT Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Val 305 310 315	963
GAG AAC GGC AAA ACC GGA GTG AGT TTG TCC AAG GAC ATA ACC GAT GTT Glu Asn Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val 320 325 330	1011

GCT GGT CGA ACG GTT AAG AAA AAC ATA GCA ACG CTG GGT CCG TTG ATT		1059	
Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile			
335	340	345	350
CTT CCG TTA AGC GAG AAA CTT CTT TTT TTC GTT ACC TTC ATG GGC AAG		1107	
Leu Pro Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys			
355	360	365	
AAA CTT TTC AAA GAC AAA ATC AAA CAT TAT TAC GTC GTC CCG GAC TTC AAG		1155	
Lys Leu Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys			
370	375	380	
CTT GCT ATC GAC CAT TTT TGT ATA CAT GCC GGA GGC AAA GCC GTG ATT		1203	
Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile			
385	390	395	
GAT GTG CTA GAG AAG AAC CTA GGC CTA GCA CCG ATC GAT GTA GAG GCA		1251	
Asp Val Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala			
400	405	410	
TCA AGA TCA ACG TTA CAT AGA TTT GGA AAC ACT TCA TCT AGC TCA ATA		1299	
Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile			
415	420	425	430
TGG TAT GAG TTG GCA TAC ATA GAA GCA AAA GGA AGG ATG AAG AAA GGT		1347	
Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly			
435	440	445	
AAT AAA GTT TGG CAG ATT GCT TTA GGG TCA GGC TTT AAG TGT AAC AGT		1395	
Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser			
450	455	460	
GCA GTT TGG GTG GCT CTA AAC AAT GTC AAA GCT TCC AAA TAGGATCC		1442	
Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys			
465	470	475	

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19 :

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GTCGACAAA ATG ACG TCC ATT AAC GTA AAG CTC CTT TAC CAT TAC GTC ATA 51
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile
    1           5           10

ACC AAC CTT TTC AAC CTT TGC TTC TTT CCG TTA ACG GCG ATC GTC GCC 99
Thr Asn Leu Phe Asn Leu Cys Phe Pro Leu Thr Ala Ile Val Ala
    15          20          25          30

GGA AAA GCC TAT CGG CTT ACC ATA GAC GAT CTT CAC CAC TTA TAC TAT 147
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr
    35          40          45

TCC TAT CTC CAA CAC AAC CTC ATA ACC ATC GCT CCA CTC TTT GCC TTC 195
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe
    50          55          60

ACC GTT TTC GGT TCG GTT CTC TAC ATC GCA ACC CGG CCC AAA CCG GTT 243
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val
    65          70          75

TAC CTC GTT GAG TAC TCA TGC TAC CTT CCA CCA ACG CAT TGT AGA TCA 291
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser
    80          85          90

AGT ATC TCC AAG GTC ATG GAT ATC TTT TAT CAA GTA AGA AAA GCT GAT 339
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp
    95          100         105         110

CCT TCT CGG AAC GGC ACG TGC GAT GAC TCG TCG TGG CTT GAC TTC TTG 387
Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu
   115          120         125

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AGG AAG ATT CAA GAA CGT TCA GGT CTA GGC GAT GAA ACT CAC GGG CCC Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro 130	135	140	435
GAG GGG CTG CTT CAG GTC CCT CCC CGG AAG ACT TTT GCG GCG GCG CGT Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg 145	150	155	483
GAA GAG ACG GAG CAA GTT ATC ATT GGT GCG CTA GAA AAT CTA TTC AAG Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys 160	165	170	531
AAC ACC AAC GTT AAC CCT AAA GAT ATA GGT ATA CTT GTG GTG AAC TCA Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser 175	180	185	579
AGC ATG TTT AAT CCA ACT CCA TCG CTC TCC GCG ATG GTC GTT AAC ACT Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr 195	200	205	627
TTC AAG CTC CGA AGC AAC GTA AGA AGC TTT AAC CTT GGT GGC ATG GGT Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Met Gly 210	215	220	675
TGT AGT GCC GGC GTT ATA GCC ATT GAT CTA GCA AAG GAC TTG TTG CAT Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His 225	230	235	723
GTC CAT AAA AAT ACG TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr 240	245	250	771
TAT AAC ATT TAC GCT GGT GAT AAT AGG TCC ATG ATG GTT TCA AAT TGC Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys 255	260	265	819
TTG TTC CGT GTT GGT GGG GCC GCT ATT TTG CTC TCC AAC AAG CCT GGA Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly 275	280	285	867
GAT CGT AGA CGG TCC AAG TAC GAG CTA GTT CAC ACG GTT CGA ACG CAT Asp Arg Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His 290	295	300	915

ACC GGA GCT GAC GAC AAG TCT TTT CGT TGC GTG CAA CAA GGA GAC GAT		963
Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp		
305	310	315
GAG AAC GGC AAA ATC GGA GTG AGT TTG TCC AAG GAC ATA ACC GAT GTT		1011
Glu Asn Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val		
320	325	330
GCT GGT CGA ACG GTT AAG AAA AAC ATA GCA ACG TTG GGT CCG TTG ATT		1059
Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile		
335	340	345
350		
CTT CCG TTA AGC GAG AAA CTT CTT TTT TTC GTT ACC TTC ATG GGC AAG		1107
Leu Pro Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys		
355	360	365
AAA CTT TTC AAA GAT AAA ATC AAA CAT TAC TAC GTC CCG GAT TTC AAA		1155
Lys Leu Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys		
370	375	380
CTT GCT ATT GAC CAT TTT TGT ATA CAT GCC GGA GGC AGA GCC GTG ATT		1203
Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile		
385	390	395
GAT GTG CTA GAG AAG AAC CTA GCC CTA GCA CCG ATC GAT GTA GAG GCA		1251
Asp Val Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala		
400	405	410
TCA AGA TCA ACG TTA CAT AGA TTT GGA AAC ACT TCA TCT AGC TCA ATA		1299
Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile		
415	420	425
430		
TGG TAT GAG TTG GCA TAC ATA GAA GCA AAA GGA AGG ATG AAG AAA GGT		1347
Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly		
435	440	445
AAT AAA GTT TGG CAG ATT GCT TTA GGG TCA GGC TTT AAG TGT AAC AGT		1395
Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser		
450	455	460

GCA GTT TGG GTG GCT CTA AAC AAT GTC AAA GCT TCC AAA TAGGATCC 1442
Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys
465 470 475

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 :

AAG CTT AAA CTA GTG TAT CAT TAC CTA ATC TCC AAC GCT CTC TAC ATC 48
Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Leu Tyr Ile
1 5 10 15

CTC CTC CTT CCT CTC CTC GCC GCA ACA ATC GCT AAC CTC TCT TCT TTC 96
Leu Leu Leu Pro Leu Leu Ala Ala Thr Ile Ala Asn Leu Ser Ser Phe
20 25 30

ACC ATC AAC GAC CTC TCT CTC CTC TAC AAC ACA CTC CGT TTC CAT TTC 144
Thr Ile Asn Asp Leu Ser Leu Leu Tyr Asn Thr Leu Arg Phe His Phe
35 40 45

CTC TCC GCC ACA CTC GCC ACC GCA CTC TTG ATC TCT CTC TCC ACC GCT 192
Leu Ser Ala Thr Leu Ala Thr Ala Leu Leu Ile Ser Leu Ser Thr Ala
50 55 60

TAC TTC ACC ACC CGT CCT CGC CGT GTC TTC CTC CTC GAC TTC TCG TGT 240
Tyr Phe Thr Thr Arg Pro Arg Arg Val Phe Leu Leu Asp Phe Ser Cys
65 70 75 80

TAC AAA CCA GAC CCT TCA CTG ATC TGC ACT CGT GAA ACA TTC ATG GAC 288
Tyr Lys Pro Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp
85 90 95

AGA TCT CAA CGT GTA GGC ATC TTC ACA GAA GAC AAC TTA GCT TTC CAA	336
Arg Ser Gln Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln	
100	105
	110
CAA AAG ATC CTC GAA AGA TCC GGT CTA GGT CAG AAA ACT TAC TTC CCT	384
Gln Lys Ile Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro	
115	120
	125
GAA GCT CTT CTT CGT GTT CCT CCT AAT CCT TGT ATG GAA GAA GCG AGA	432
Glu Ala Leu Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg	
130	135
	140
AAA GAG GCA GAA ACA GTT ATG TTC GGA GCT ATT GAC GCG GTT CTT GAG	480
Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile Asp Ala Val Leu Glu	
145	150
	155
	160
AAG ACC GGT GTG AAA CCT AAA GAT ATT GGA ATC CTT GTG GTG AAT TGT	528
Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys	
165	170
	175
AGC TTG TTT AAT CCA ACA CCG TCA CTT TCT GCT ATG ATT GTG AAT AAG	576
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys	
180	185
	190
TAT AAG CTT AGA GGC AAC ATT TTG AGC TAT AAT TTC GGC GGG ATG GG	623
Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Phe Gly Gly Met Gly	
195	200
	205

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 :

AAG CTT AAG TTA GGC TAC CAC TAT CTG ATC ACT CAC TTT TTT AAA CTC Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Phe Phe Lys Leu	1 5 10 15	48
ATG TTC CTC CCT CTA ATG GCT GTT TTG TTC ATG AAT GTC TCA TTG TTA Met Phe Leu Pro Leu Met Ala Val Leu Phe Met Asn Val Ser Leu Leu	20 25 30	96
AGC CTA AAC CAT CTT CAG CTC TAT TAC AAT TCC ACC GGA TTC ATC TTC Ser Leu Asn His Leu Gln Leu Tyr Tyr Asn Ser Thr Gly Phe Ile Phe	35 40 45	144
GTC ATC ACT CTC GCC ATT GTC GGA TCC ATT GTC TTC TTC ATG TCT CGA Val Ile Thr Leu Ala Ile Val Gly Ser Ile Val Phe Phe Met Ser Arg	50 55 60	192
CCT AGA TCC ATC TAC CTT CTA GAT TAC TCT TGC TAC CTC CCG CCT TCG Pro Arg Ser Ile Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro Pro Ser	65 70 75 80	240
AGT CAA AAA GTT AGC TAC CAG AAA TTC ATG AAC AAC TCT AGT TTG ATT Ser Gln Lys Val Ser Tyr Gln Lys Phe Met Asn Asn Ser Ser Leu Ile	85 90 95	288
CAA GAT TTC AGC GAA ACT TCT CTT GAG TTC CAG AGG AAG ATC TTG ATT Gln Asp Phe Ser Glu Thr Ser Leu Glu Phe Gln Arg Lys Ile Leu Ile	100 105 110	336
CGC TCT GGT CTC GGT GAA GAG ACT TAT TTA CCG GAT TCT ATT CAC TCT Arg Ser Gly Leu Gly Glu Thr Tyr Leu Pro Asp Ser Ile His Ser	115 120 125	384
ATC CCT CCG CGT CCT ACT ATG GCT GCA GCG CGT GAA GAA GCG GAG CAG Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ala Glu Gln	130 135 140	432
GTA ATC TTC GGT GCA CTC GAC AAT CTT TTC GAG AAT ACA AAA ATC AAT Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys Ile Asn	145 150 155 160	480

CCT AGG GAG ATT GGT GTT CTT GTG AAT TGT AGT TTG TTT AAC CCC 528
Pro Arg Glu Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn Pro
165 170 175

ACG CCT TCT TTA TCC GCC ATG ATT GTT AAC AAG TAT AAG CTT AGA GGA 576
Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly
180 185 190

AAC ATT AAG AGC TTT AAT CTC GGC GGC ATG G 607
Asn Ile Lys Ser Phe Asn Leu Gly Gly Met
195 200

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAG CTT AAA CTG GGG TAC CAC TAC CTC ATT ACT CAT CTC TTC AAG CTC Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Leu Phe Lys Leu 1 5 10 15	48
TGT TTG GTT CCA TTA ATG GCG GTT TTA GTC ACA GAG ATC TCC CGA TTA Cys Leu Val Pro Leu Met Ala Val Leu Val Thr Glu Ile Ser Arg Leu 20 25 30	96
ACA ACA GAC GAT CTT TAC CAG ATT TGC CTT CAT CTC CAA TAC AAT CTC Thr Thr Asp Asp Leu Tyr Gln Ile Cys Leu His Leu Gln Tyr Asn Leu 35 40 45	144
GTT GCT TTC ATC TTT CTC TCT GCT TTA GCT ATC TTT GGC TCC ACC GTT Val Ala Phe Ile Phe Leu Ser Ala Leu Ala Ile Phe Gly Ser Thr Val 50 55 60	192
TAC ATC ATG AGT CGT CCC AGA TCT GTT TAT CTC GTT GAT TAC TCT TGT Tyr Ile Met Ser Arg Pro Arg Ser Val Tyr Leu Val Asp Tyr Ser Cys 65 70 75 80	240
TAT CTT CCT CCG GAG AGT CTT CAG GTT AAG TAT CAG AAG TTT ATG GAT Tyr Leu Pro Pro Glu Ser Leu Gln Val Lys Tyr Gln Lys Phe Met Asp 85 90 95	288
CAT TCT AAG TTG ATT GAA GAT TTC AAT GAG TCA TCT TTA GAG TTT CAG His Ser Lys Leu Ile Glu Asp Phe Asn Glu Ser Ser Leu Glu Phe Gln 100 105 110	336
AGG AAG ATT CTT GAA CGT TCT GGT TTA GGA GAA GAG ACT TAT CTC CCT Arg Lys Ile Leu Glu Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro 115 120 125	384
GAA GCT TTA CAT TGT ATC CCT CCG AGG CCT ACG ATG ATG GCG GCT CGT Glu Ala Leu His Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg 130 135 140	432
GAG GAA GCT GAG CAG GTA ATG TTT GGT GCT CTT GAT AAG CTT TTC GAG Glu Glu Ala Glu Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu 145 150 155 160	480

AAT ACC AAG ATT AAC CCT AGG GAT ATT GGT GTG TTG GTT GTG AAT TGT 528
Asn Thr Lys Ile Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys
165 170 175

AGC TTG TTT AAT CCT ACA CCT TCG TTG TCA GCT ATG ATT GTT AAC AAG 576
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
180 185 190

TAT AAG CTT AGA GGG AAT GTT AAG AGT TTT AAC CTG GGG GGC ATT G 622
Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Ile
195 200 205

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 :

AAG CTT AAG TTA TGG TAT CAC TAC CTG ATT TCT CAC CTT TTT AAG CTC 48
Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu
1 5 10 15

TTG TTG GTT CCT TTA ATG GCG GTT CTG TTC ACG AAT GTC TCC CGG TTA 96
Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu
20 25 30

AGC CTA AAC CAG CTC TGT CTC GAT CTC TCT CTC CAG CTC CAG TTC AAT 144
Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn
35 40 45

CTC GTC GGA TTC ATC TTC ATT ACC GTC TCC ATT TTC GGA TTC ACA 192
Leu Val Gly Phe Ile Phe Phe Ile Thr Val Ser Ile Phe Gly Phe Thr
50 55 60

GTT ATC TTC ATG TCC CGA CCT AGA TCC GTT TAC CTC CTC GAC TAC TCA 240
Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser
65 70 75 80

TGT TAC CTC CCG CCG TCG AAT CTC AAA GTT AGC TAC CAG ACA TTC ATG Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met 85 90 95	288
AAT CAT TCT AAA CTG ATT GAA GAT TTC GAC GAG TCG TCG CTT GAG TTC Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe 100 105 110	336
CAG CGG AAG ATC CTG AAG CGA TCC GGT CTC GGC GAA GAG ACT TAC CTC Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Thr Tyr Leu 115 120 125	384
CCG GAA TCT ATC CAC TGC ATC CCG CCG CGT CCG ACT ATG GCG GCG GCG Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala 130 135 140	432
CGT GAG GAA TCG GAG CAG GTA ATC TTC GGT GCA CTC GAC AAT CTC TTC Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe 145 150 155 160	480
GAG AAT ACC AAA ATC GAC CCT AGG GAG ATT GGT GTT GTG GTG GTG AAC Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn 165 170 175	528
TGC AGC TTG TTT AAC CCG ACG CCT TCT TTA TCC GCC ATG ATT GTG AAC Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn 180 185 190	576
AAG TAT AAG CTT AGA GGA AAC GTG AAG AGC TTT AAT CTC GGT GGC ATG G Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met 195 200 205	625

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTG AAG CGA TCC GGT CTC GGC GAA GAG ACT TAC CTC CCG GAA TCT ATC Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Glu Ser Ile 135 140 145	488
CAC TGC ATC CCG CCG CGT CCG ACT ATG GCG GCG CGT GAG GAA TCG His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ser 150 155 160 165	536
GAG CAG GTA ATC TTC GGT GCA CTC GAC AAT CTC TTC GAG AAT ACC AAA Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys 170 175 180	584
ATC GAC CCT AGG GAG ATT GGT GTT GTG GTG AAC TGC AGC TTG TTT Ile Asp Pro Arg Glu Ile Gly Val Val Val Asn Cys Ser Leu Phe 185 190 195	632
AAC CCG ACG CCT TCT TTA TCC GCC ATG ATT GTG AAC AAG TAT AAG CTT Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu 200 205 210	680
AGA GGA AAC GTG AAG AGC TTT AAC CTC GGA GGA ATG GGA TGT AGG GCT Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Arg Ala 215 220 225	728
GGT GTC ATC GCC GTT GAT CTC GCT AAT GAC ATT TTA CAG CTC CAT AGA Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile Leu Gln Leu His Arg 230 235 240 245	776
AAC ACA TTA GCT CTT GTG GTT AGC ACA GAG AAC ATC ACT CAG AAT TGG Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp 250 255 260	824
TAC TTT GGT AAC AAC AAA GCA ATG TTG ATT CCT AAT TGC TTG TTT AGG Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg 265 270 275	872
GTT GGT GGA TCC GCG GTT CTG CTT TCG AAC AAG CCT CGT GAT CGA AAA Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Pro Arg Asp Arg Lys 280 285 290	920
CGA TCC AAG TAT AAA CTT GTT CAC ACG GTA CGG ACT CAT AAA GGA TCT Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ser 295 300 305	968

GAT GAG AAA GCA TTC AAC TGT GTG TAC CAA GAA CAA GAC GAG GAC TTG Asp Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu Gln Asp Glu Asp Leu 310 315 320 325	1016
AAA ACC GGA GTT TCT TTG TCT AAA GAC CTA ATG TCT ATA GCT GGA GAA Lys Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ser Ile Ala Gly Glu 330 335 340	1064
GCT CTA AAG ACA AAT ATC ACC ACT TTG GGT CCT CTG GTT CTT CCA ATA Ala Leu Lys Thr Asn Ile Thr Leu Gly Pro Leu Val Leu Pro Ile 345 350 355	1112
AGC GAG CAG ATT CTG TTC ATT GCG ACT TTT GTT GCA AAG AGA TTG TTC Ser Glu Gln Ile Leu Phe Ile Ala Thr Phe Val Ala Lys Arg Leu Phe 360 365 370	1160
AGT GCC AAG AAG AAG AAG AAG CCT TAC ATA CCG GAT TTC AAG CTT Ser Ala Lys Lys Lys Lys Pro Tyr Ile Pro Asp Phe Lys Leu 375 380 385	1208
GCC TTT GAT CAT TTC TGT ATT CAC GCA GGA GGT AGA GCC GTG ATC GAT Ala Phe Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp 390 395 400 405	1256
GAA CTA GAG AAG AGT TTA AAG CTA TTG CCA AAA CAT GTG GAG GCT TCT Glu Leu Glu Lys Ser Leu Lys Leu Leu Pro Lys His Val Glu Ala Ser 410 415 420	1304
AGA ATG ACA TTG CAT AGA TTT GGA AAC ACT TCA TCG AGC TCT ATT TGG Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp 425 430 435	1352
TAT GAA TTA GCT TAC ACA GAA GCT AAA GGA AGA ATG AGA AAA GGG AAT Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg Met Arg Lys Gly Asn 440 445 450	1400
CGA GTT TGG CAG ATT GCT TTT GGA AGC GGC TTT AAG TGT AAC AGC GCG Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala 455 460 465	1448

GTT TGG GTG GCT CTT CGT GAT GTC GAG CCC TCG GTT AAC AAT CCT TGG 1496
Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp
470 475 480 485

GAA CAT TGC ATC CAT AGA TAT CCG GTT AAG ATC GAT CTC TGATTCAGC 1545
Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu
490 495

TTAACCGGTA AAATTGGTCT GTACATATAT TTACCACTGA GTAAAGACAT CAGTTAATGA 1605

TTTGTGTTA CTCAATTGGG CTAAGTGTAT TATTATATGT GTTGTATATA ATAAAGGTAG 1665

AACGTAAATT TACTAAGAAA AAAAAAAA AAAAAAAA 1704

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CA ATG ACG TCT GTG AAC GTA AAA CTC CTT TAC CAT TAC GTC ATA ACC 47
Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr
1 5 10 15

AAC TTT TTC AAC CTC TGT TTC CCA CTG ACG GGG ATC CTC GCC GGA 95
Asn Phe Phe Asn Leu Cys Phe Pro Leu Thr Gly Ile Leu Ala Gly
20 25 30

AAA GGC TCT CGT CTT ACC ACA AAC GAT CTC CAC CAC TTC TAT TCA TAT 143
Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr
35 40 45

CTC CAA CAC AAN CTT ATA ACC TTA ACC CTA CTC TTT GGC TTC ACC GTT Leu Gln His Xxx Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val	50	55	60	191
TTT GGT TCG GTT CTC TAC TTC GTA ANC CGA CCC AAA CCG GTT TAC CTC Phe Gly Ser Val Leu Tyr Phe Val Xxx Arg Pro Lys Pro Val Tyr Leu	65	70	75	239
GTT GAC TAC TCC TGC TAC CTT CCA CCA CAA CAT CTT AGC GCT GGT ATC Val Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile	80	85	90	287
TCT AAG ACC ATG GAA ATC TTT TAT CAA ATA AGA AAA TCT GAT CCT TTA Ser Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu	100	105	110	335
CGA AAC GTG GCA TTA GAT GAT TCG TCT TCT CTT GAT TTC TTG AGA AAG Arg Asn Val Ala Leu Asp Asp Ser Ser Leu Asp Phe Leu Arg Lys	115	120	125	383
ATT CAA GAG CGT TCA GGT CTA GGC GAT GAA ACC TAC GGC CCC GAG GGA Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly	130	135	140	431
CTG TTT GAG ATT CCT CCG AGG AAG AAT TTA GCG TCG GCG CGT GAA GAG Leu Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu	145	150	155	479
ACG GAG CAA GTA ATC AAC GGT GCG CTA AAA AAT CTA TTC GAG AAC AAC Thr Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn	160	165	170	527
AAA GTT AAC CCT AAA GAG ATT GGT ATA CTT GTG GTG AAC TCA AGC ATG Lys Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	180	185	190	575
TTT AAT CCG ACT CCT TCG TTA TCC GCG ATG GTA GTT AAT ACT TCC AAG Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys	195	200	205	623

CTC CGA AGC AAC ATC AAA AGC TTT AAT CTT GGA GGA ATG GGT TGC AGT 671
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

 GCT GGT GTT ATC GCC ATT GAT CTA GCT AAA GAC TTG TTG CAT GTT CAT 719
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235

 AAA AAC ACA TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT CAA AAC 767
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn
 240 245 250 255

 ATT TAT ACC GGT GAT AAC AGA TCC ATG ATG GTT TCG AAT TGC TTG TTC 815
 Ile Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270

 CGT GTC GGT GGG GCA GCG ATT CTG CTC TCC AAC AAG CCG GGG GAT CGA 863
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285

 AGA CGG TCC AAG TAC AAG CTA GCT CAC ACG GTT CGA ACG CAT ACC GGA 911
 Arg Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly
 290 295 300

 GCT GAC GAC AAG TCT TTT GGA TGT GTG CGG CAA GAA GAA GAT GAT AGC 959
 Ala Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser
 305 310 315

 GGT AAA ACC GGA GTT AGT TTG TCA AAA GAC ATA ACC GTT GTT GCC GGG 1007
 Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly
 320 325 330 335

 ATA ACG GTT CAG AAA AAC ATA ACA ACA TTG GGT CCG TTG GTT CTT CCT 1055
 Ile Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro
 340 345 350

 CTG AGC GAA AAA ATC CTT TTT GTC GTT ACA TTC GTA GCC AAG AAA CTA 1103
 Leu Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu
 355 360 365

 TTA AAA GAT AAG ATC AAA CAC TAT TAC GTG CCG GAT TTC AAA CTT GCA 1151
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

GTA GAT CAT TTC TGT ATT CAT GCG GGA GGT AGA GCC GTG ATA GAT GTG Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385	390	395	1199
TTA GAG AAG AAC TTA GGG CTA TCG CCG ATA GAT GTG GAG GCA TCA AGA Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg 400	405	410	1247
TCA ACA TTA CAT AGA TTT GGG AAT ACA TCG TCT AGT TCA ATT TGG TAT Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr 420	425	430	1295
GAA TTA GCA TAC ATA GAG CCA AAA GGA AGG ATG AAG AAA GGT AAT AAA Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys 435	440	445	1343
GCT TGC CAA ATA GCT GGT GGG TCA GGT TTT AAG TGT AAT AGT GCG GTT Ala Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450	455	460	1391
TGG GTC GCT TTA CGC AAT GTC GAG GCT TCA GCT AAT AGT CCT TGG GAA Trp Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu 465	470	475	1439
CAT TGC ATT CAC AAA TAT CCG GTT CAA ATG TAT TCT GGT TCA TCA AAG His Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys 480	485	490	1487
TCA GAG ACT CCT GTC CAA AAC GGT CGG TCC TAATTTATGT ATCTCAAATG Ser Glu Thr Pro Val Gln Asn Gly Arg Ser 500			1537
ATGTTGTCCA CTTTCTCTTT TTTTTTTCT TTTTTTAGTT ATAATTAAAT GGTTACGATG			1597
TTTTGTCTAG GTCGTTATAA ATAAAGAATA CATGGGTGTT ACTAGTATAA AAAAAAAA			1657
AAAAAAAA			1664

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTTTCTTCTT CCCCAACA ATG ACC CAT AAC CAA AAC CAA CCT CAC CGG GCA Met Thr His Asn Gln Asn Gln Pro His Arg Ala	51
1 5 10	
GTT CCG GTT CAC GTT ACA AAC TCC GAT CAA AAC CAA AAC CAA AAC CAA Val Pro Val His Val Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln	99
15 20 25	
AAC AAT CTC CCA AAT TTT CTC TTA TCT GTT CGG CTC AAA TAT GTA AAA Asn Asn Leu Pro Asn Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys	147
30 35 40	
CTT GGG TAC CAT TAC CTA ATC TCC AAC GGT CTC TAC ATC CTC CTC CTC Leu Gly Tyr His Tyr Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu	195
45 50 55	
CCT CTC CTC GGC GGC ACA ATC GTA AAA CTC TCT TCC TTC ACA CTC AAC Pro Leu Leu Gly Gly Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn	243
60 65 70 75	
GAA CTC TCT CTC CTC TAC AAC CAC CTC CGT TTT CAT TTC CTC TCC GCC Glu Leu Ser Leu Leu Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala	291
80 85 90	
ACA CTC GCT ACC GGA CTC TTA ATC TCT CTC TCC ACC GCC TAC TTC ACC Thr Leu Ala Thr Gly Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr	339
95 100 105	
ACC CGT CCT CGT CAT GTC TTC CTC CTC GAC TTC TCA TGC TAC AAA CCT Thr Arg Pro Arg His Val Phe Leu Leu Asp Phe Ser Cys Tyr Lys Pro	387
110 115 120	

GAC CCT TCC TTA ATA TGC ACT CGT GAA ACA TTC ATG GAC CGA TCT CAA Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp Arg Ser Gln 125 130 135	435
CGT GTA GGT ATC TTC ACA GAA GAC AAC CTC GCT TTT CAA CAA AAG ATC Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln Gln Lys Ile 140 145 150 155	483
CTC GAA AGA TCC GGT CTT GGG CAG AAA ACT TAC TTC CCT GAA GCT CTT Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro Glu Ala Leu 160 165 170	531
CTT CGT GTT CCT CCC AAT CCT TGT ATG GAA GAA GCG AGA AAA GAA GCA Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg Lys Glu Ala 175 180 185	579
GAG ACT GTT ATG TTC GGA GCT ATA GAC TCT GTT CTT GAG AAA ACC GGT Glu Thr Val Met Phe Gly Ala Ile Asp Ser Val Leu Glu Lys Thr Gly 190 195 200	627
GTG AAA CCT AAA GAT ATC GGA ATC CTT GTC GTG AAT TGT AGT TTG TTT Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe 205 210 215	675
AAT CCG ACG CCG TCA CTT TCC GCC ATG ATT GTG AAT AAG TAT AAG CTT Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu 220 225 230 235	723
AGA GGA AAC ATT TTG AGC TAT AAT CTC GGT GGA ATG GGT TGT AGT GCT Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala 240 245 250	771
GGA CTT ATC TCC ATT GAT CTC GCT AAA CAG CTT CTT CAG GTC CAA CCA Gly Leu Ile Ser Ile Asp Leu Ala Lys Gln Leu Leu Gln Val Gln Pro 255 260 265	819
AAC TCA TAC GCA CTA GTG GTG AGC ACA GAG AAC ATA ACC TTA AAC TGG Asn Ser Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp 270 275 280	867
TAC TTA GGC AAC GAC CGA TCA ATG CTT CTC TCT AAC TGC ATC TTC CGT Tyr Leu Gly Asn Asp Arg Ser Met Leu Leu Ser Asn Cys Ile Phe Arg 285 290 295	915

ATG GGA GGA GCC GCC GTA CTT CTC TCA AAC CGT TCC TCC GAT CGC ACC Met Gly Gly Ala Ala Val Leu Leu Ser Asn Arg Ser Ser Asp Arg Thr 300 305 310 315	963
CGT TCA AAA TAT CAG CTC ATC CAC CCC GTC CGT ACC CAC AAA GGA GCC Arg Ser Lys Tyr Gln Leu Ile His Pro Val Arg Thr His Lys Gly Ala 320 325 330	1011
AAC GAC AAC GCA TTT GGC TGC GTT TAC CAA CGA GAA GAC AAC AAC GAA Asn Asp Asn Ala Phe Gly Cys Val Tyr Gln Arg Glu Asp Asn Asn Glu 335 340 345	1059
GAA GAA ACC GCC AAA ATC GGA GTC TCA CTC TCT AAA AAC CTA ATG GCA Glu Glu Thr Ala Lys Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala 350 355 360	1107
ATA GCC GGA GAA GCT CTC AAG ACA AAC ATA ACA ACA CTC GGA CCA CTA Ile Ala Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu 365 370 375	1155
GTC TTA CCA ATG TCC GAA CAG ATT CTG TTT TTC CCA ACA CTC GTG GCT Val Leu Pro Met Ser Glu Gln Ile Leu Phe Phe Pro Thr Leu Val Ala 380 385 390 395	1203
CGA AAA ATC TTC AAA GTC AAG AAA ATA AAG CCT TAC ATA CCC GAT TTC Arg Lys Ile Phe Lys Val Lys Ile Lys Pro Tyr Ile Pro Asp Phe 400 405 410	1251
AAG CTA GCT TTC GAG CAT TTC TGC ATC CAT GCG GGA GGT AGA GCA GTG Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala Val 415 420 425	1299
CTT GAT GAG ATA GAG AAG AAT TTG GAT TTA TCA GAG TGG CAT ATG GAA Leu Asp Glu Ile Glu Lys Asn Leu Asp Leu Ser Glu Trp His Met Glu 430 435 440	1347
CCA TCG AGG ATG ACT TTA AAC CGG TTT GGT AAT ACT TCG AGT AGC TCA Pro Ser Arg Met Thr Leu Asn Arg Phe Gly Asn Thr Ser Ser Ser 445 450 455	1395
CTT TGG TAT GAA CTT GCG TAT AGT GAA GCT AAA GGG AGG ATT AAG AGA Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg 460 465 470 475	1443

GGA GAT AGG ACT TGC CAA ATT GCG TTT GGA TCG GGA TTT AAG TGT AAT Gly Asp Arg Thr Cys Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn 480 485 490	1491
AGT GCG GTT TGG AAA GCT TTG AGA ACC ATT GAT CCT ATT GAT GAG AAG Ser Ala Val Trp Lys Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys 495 500 505	1539
AAG AAT CCA TGG AGT GAT GAG ATT CAT GAG TTT CCA GTT TCT GTT CCT Lys Asn Pro Trp Ser Asp Glu Ile His Glu Phe Pro Val Ser Val Pro 510 515 520	1587
AGG ATC ACT CCA GTT ACT TCT AAC TAGTGTTTTT TTTTTGGGTC CAACTAGGGA 1641 Arg Ile Thr Pro Val Thr Ser Asn 525 530	
TAATATTGT TATGGTTTG TTCTTACGTA CGTACTTAA GTGATTTAGT CTAAAAATAA 1701	
ATTGGTTTCA TAAAAAAAAA AAAAAAAAAA A	1732

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27 :

AAG CTT AAA CTA GTA TAC CAT TAC TTG ATC TCC AAC GCC ATG TAT TTG Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu 1 5 10 15	48
TTA ATG GTG CCG CTT CTA GCA GTA GCC TTT GCT CAT CTC TCC ACG TTG Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu 20 25 30	96

ACG ATT CAA GAT CTG GTT CAT CTT TGG GAA CAG CTT AAG TTC AAT TTA	144		
Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu			
35	40	45	
CTG TCA GTA ACT CTC TGC TCG AGC CTT ATG GTG TTT TTA GGG ACT CTG	192		
Leu Ser Val Thr Leu Cys Ser Ser Leu Met Val Phe Leu Gly Thr Leu			
50	55	60	
TAT TTC ATG AGC CGA CCG ACG AAG ATT TAC TTG GTG GAT TTC TCT TGT	240		
Tyr Phe Met Ser Arg Pro Thr Lys Ile Tyr Leu Val Asp Phe Ser Cys			
65	70	75	80
TAC AAG CCG GAA AAA GAG CGT ATA TGC ACG AGA GAG ATT TTC TAT GAG	288		
Tyr Lys Pro Glu Lys Glu Arg Ile Cys Thr Arg Glu Ile Phe Tyr Glu			
85	90	95	
AGA TCG AAA CTA ACT GGG AAT TTT ACC GAT GAT AAT TTA ACT TTC CAA	336		
Arg Ser Lys Leu Thr Gly Asn Phe Thr Asp Asp Asn Leu Thr Phe Gln			
100	105	110	
AAG AAA ATT ATC GAA AGA TCT GGA TTA GGT CAG AAC ACG TAC TTA CCT	384		
Lys Lys Ile Ile Glu Arg Ser Gly Leu Gly Gln Asn Thr Tyr Leu Pro			
115	120	125	
GAG GCC GTT CTA CGG GTT CCG CCC AAT CCG TGT ATG GCG GAG GCT AGA	432		
Glu Ala Val Leu Arg Val Pro Pro Asn Pro Cys Met Ala Glu Ala Arg			
130	135	140	
AAG GAG GCT GAG ATG GTT ATG TTC GGT GCG ATC GAT GAA TTG TTG GAG	480		
Lys Glu Ala Glu Met Val Met Phe Gly Ala Ile Asp Glu Leu Leu Glu			
145	150	155	160
AAA ACC GGG GTT AAA CCT AAG GAT ATC GGT ATT CTT GTG GTG AAT TGC	528		
Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys			
165	170	175	
AGC TTG TTC AAT CCG ACG CCG TCT CTG TCC GCA ATG GTG GTT AAT CGG	576		
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Arg			
180	185	190	
TAC AAG CTT AGA GGG AAT ATC ATA AGT TAT AAC CTT GGC GGG ATG G	622		
Tyr Lys Leu Arg Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met			
195	200	205	

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 :

Asn Ile Thr Thr Leu Gly
5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 :

Ser Asn Cys Lys Phe Gly
5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAUCAUCAUC AUGTCGACAA AATGACGTCC ATTAACGTAA AG

42

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :

CUACUACUAC UAGTCGACGG ATCCTATTG GAAGCTTG CATTGTTAG

50

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE: Xaa at position 3 = Leu or Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Lys Leu Xaa Tyr His Tyr

5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

CAUCAUCAUC AUGAATTCAA GCTTAARYTN BKNTAYCAYT A

41

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Asn Leu Gly Gly Met Gly Cys
5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

CAUCAUCAUC AUGAATTCAA GCTTAAYYTN GGNGGNATGG G

41

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

CUACUACUAC UAGGATCCGT CGACCCATNC CNCCNARRTT

40

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Gly Phe Lys Cys Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other
(A) DESCRIPTION: synthetic oligonucleotide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :
CUACUACUAC UAGGATCCGT CGACSWRTTR CAYTTRAANC C

41

(2) INFORMATION FOR SEQ ID NO: 39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other
(A) DESCRIPTION: synthetic oligonucleotide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :
CUACUACUAC UASWRTTRCA YTTRAANCC

29